

111. (new) A method of claim 93 wherein said nucleic acid sequence is a *Mycobacterium xenopi*-specific sequence comprising a 16S-23S rRNA spacer sequence of SEQ ID NO: 163.

BY  
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112. (new) A method of claim 93 wherein said nucleic acid sequence is a *Mycobacterium celatum*-specific sequence comprising a 16S-23S rRNA spacer sequence of SEQ ID NO: 170.

113. (new) Method according to any one of claims claim 93-112 wherein said detecting comprises sequence analysis of said nucleic acid.

114. (new) Method according to any one of claims 93-112 wherein said detecting comprises hybridizing a taxon-specific probe to said nucleic acid, said probe specifically hybridizing with the 16S-23S rRNA spacer sequence.--

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#### REMARKS

Entry of the above is requested.

Claims 54-114 are pending. Claims 89-114 have been added. No new matter has been added.

Claim 54 has been amended to include RNA forms, such as are described, for example, at page 13, lines 15-18, of the specification.

The specification has been amended to correct an inadvertent typographical error. Support for the amendment may be found, for example, in Table 10 on page 102. No new matter has been added.

The restriction requirement should be withdrawn as a search of all the claimed subject matter is not believed to present an undue burden on the Examiner.

At a minimum, the Examiner is requested to issue a further Office Action restricting the claims in a manner consistent with the restriction requirement received from the present Examiner in the grand-parent application (Serial No. 09/765,332 - now U.S. Patent No. 6,025,132) in the Office Action dated June 17, 1998 (Paper No. 9) (copy attached). The applicants were granted protection in the grand-parent patent to a number of sequences relating to organisms found in the respiratory tract. See, attached copy of face and claims of U.S. Patent No. 6,025,132.

The applicants filed a divisional application (i.e., parent application no. 09/448,894) and received grant of U.S. Patent No. 6,312,903, also from the present Examiner, with claims relating to organisms found in a food sample. See, attached copy of face and claims of U.S. Patent No. 6,312,903.

The applicants filed the present application with the prior restriction requirement in mind and have planned to pursue claims relating to organisms of the respiratory tract (i.e., *Mycobacterium*, *Mycoplasma pneumoniae*, *Pseudomonas*, *Staphylococcus*, *Acinetobacter* and *Streptococcus*). The applicants note in this regard that claims 55, 60-73, 82, 83, 86, and 89-114 relate to organisms of the respiratory tract. Examination of claims 55, 60-73, 82, 83, 86, and 89-114, to the extent they relate to organisms of the respiratory tract, is requested.

The Examiner was understood to believe during a teleconference with the undersigned on November 21, 2002, that the restriction in the present application to a single sequence or closely related group of sequences was appropriate in the present application where the claims were directed to nucleic acid sequences *per se*. The Examiner was understood to believe that the present application presented different

issues with regard to patentability as compared to the restriction requirement of the parent and grand-parent application wherein methods were being claimed. The undersigned has reviewed the record of the grand-parent application however and the Examiner is urged to appreciate that the originally-filed claims of the grand-parent application included, as claims 46 and 47 (as also originally-field in the present application), claims to nucleic acid sequences *per se*. The Examiner in the original restriction requirement of September 5, 1997 however in the grand-parent application (copy attached) allowed for examination of sequences specific for and methods relating to 5 of the 29 enumerated organisms. Accordingly, the Examiner has previously indicated that the recitation of and claims to sequences *per se*, were not separately patentable. Similar treatment in the present application is requested for consistency and in the interests of efficient prosecution.

The applicants elect, with traverse, the subject matter of the Examiner's Group I for further prosecution in the above. The applicants elect, as a specifically disclosed sequence, SEQ ID NO: 111.

In the event the Examiner continues to believe an election of a specific sequence or set of limited number of sequences is required (see, page 3 of the Office Action of July 23, 2002 (Paper No. 5)), the Examiner is requested to examine the following 14 SEQ ID NOs: 111-115, 126, 139-146, which relate to *Pseudomonas aeruginosa*, *Acinetobacter baumannii*, *Staphylococcus* species, and *Streptococcus* species.

Alternatively, the Examiner is requested to at least allow examination of SEQ ID NOs: 111-115, which relate to *Pseudomonas* sequences.

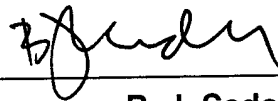
Withdrawal of the restriction requirement is requested. In the event the Examiner continues to believe a restriction requirement is appropriate, the Examiner is requested to issue a new restriction requirement consistent with the attached requirement dated June 17, 1998, received in the grand-parent application. Alternatively, a new Office Action consistent with the attached restriction requirement of September 5, 1997, from the grand-parent application is requested.

The above is believed to be completely responsive to the Office Action of July 23, 2002. The Examiner is requested to contact the undersigned however in the event anything further is required.

Respectfully submitted,

**NIXON & VANDERHYE P.C.**

By: \_\_\_\_\_



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**MARKED UP SPECIFICATION**

**IN THE SPECIFICATION**

Amend the specification as follows:

Delete the paragraph on page 55, spanning lines 17-18 and insert the following therefor:

-- FIG. 73: represents the DNA sequence of the 16S-23S spacer region from [Streptococcus] Staphylococcus saprophyticus UZG CNS46 (SEQ ID NO 148)--

**IN THE CLAIMS**

Amend the claims as follows.

54. (Amended) A micro-organism-specific nucleic acid sequence comprising a 16S-23S rRNA spacer sequence selected from the group consisting of: SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 132, SEQ ID NO: 133, SEQ ID NO: 134, SEQ ID NO: 135, SEQ ID NO: 136, SEQ ID NO: 137, SEQ ID NO: 138, SEQ ID NO: 139, SEQ ID NO: 140, SEQ ID NO: 141, SEQ ID NO: 142,

SEQ ID NO: 143, SEQ ID NO: 144, SEQ ID NO: 145, SEQ ID NO: 146, SEQ ID NO: 147, SEQ ID NO: 148, SEQ ID NO: 149, SEQ ID NO: 150, SEQ ID NO: 151, SEQ ID NO: 152, SEQ ID NO: 153, SEQ ID NO: 154, SEQ ID NO: 157, SEQ ID NO: 158, SEQ ID NO: 159, SEQ ID NO: 160, SEQ ID NO: 161, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, SEQ ID NO: 167, SEQ ID NO: 168, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 172, SEQ ID NO: 173, SEQ ID NO: 174, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 111, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 163, SEQ ID NO: 170, [and] SEQ ID NO: 215,

a sequence complementary to any of the above-recited sequences; and

a sequence recited above which contains a U in place of T.

55. (Amended) A nucleic acid sequence according to claim 54, wherein said nucleic acid sequence is a respiratory tract microorganism-specific nucleic acid sequence comprising a 16S-23S rRNA spacer sequence selected from the group consisting of: SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 157, SEQ ID NO: 158, SEQ ID NO: 159, SEQ ID NO: 160, SEQ ID NO: 161, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, SEQ ID NO: 167, SEQ ID NO: 168, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 172, SEQ ID NO: 173, SEQ ID NO: 174, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 139, SEQ ID NO: 140, SEQ ID NO: 141, SEQ ID NO: 142, SEQ ID NO: 143, SEQ ID NO: 144, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 111, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 163, SEQ ID NO: 170 and SEQ ID NO: 130.

86. (Amended) Method according to claim 82 wherein said detecting comprises hybridizing a taxon-specific probe to said nucleic acid, said probe specifically hybridizing with [a] said nucleic acid sequence [16S-23S rRNA spacer sequence of claim 54].